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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/873,637

DATE: 08/07/2001

TIME: 08:24:20

Input Set : A:\Jeffrey.app

Output Set: N:\CRF3\08072001\I873637.raw

3 <110> APPLICANT: Ross, Jeffrey
 5 <120> TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN
 6 (CRD-BP) AND ITS NUCLEIC ACID SEQUENCE
 8 <130> FILE REFERENCE: 960296.95131
 10 <140> CURRENT APPLICATION NUMBER: US/09/873,637
 11 <141> CURRENT FILING DATE: 2001-06-04
 13 <160> NUMBER OF SEQ ID NOS: 46
 15 <170> SOFTWARE: PatentIn Ver. 2.0
 17 <210> SEQ ID NO: 1
 18 <211> LENGTH: 2224
 19 <212> TYPE: DNA
 20 <213> ORGANISM: Mus musculus
 22 <400> SEQUENCE: 1

23 ggggtggggtg sgtagaaagt ttgcggctcc cgccgcccgt atccacgcct atcggcatag 60
 24 gaggatatcc gcccgcgccc gcccgatcg gcattgaatg gaacagtgtc cttgccccgc 120
 25 caccgccacc atgaacaagc ttacatcgg caacctcaac gagagtgtga cccccgcaga 180
 26 cttggagaaa gtattcgcg agcacaagat ctctacagc ggccagttct tggtaaatac 240
 27 cggctacgcc ttcgtggatt gcccgcagc gcaactggcg atgaaggcca tcgaaacttt 300
 28 ctcggggaaa gtagaactgc aaggaaaacg tctagagatt gaacactcag tccccaaaaa 360
 29 acaaaggagt cggaaaatac agatccgcaa tattccacct cagctccgat gggaagtgtc 420
 30 agatagcctg ctggctcagt acggtacagt ggagaactgt gagcaagtga acactgaaag 480
 31 tgagacagcg gtgggtcaacg tcacctactc taaccgggag cagaccaggc aagctatcat 540
 32 gaagctaaat ggccatcaac tggagaacca tgccctgaag gtctctctaca tacctgatga 600
 33 gcagataaca caaggctcctg agaatgggag tctgtggaggc tttgggtctc ggggccagcc 660
 34 ccggcaaggg tcgcccgtgg cagcaggggc tccagccaag cagcagccag tggacatccc 720
 35 tctccggctc ctggtgccta cgcagtatgt aggcgtatc attggcaagg aggggtgccac 780
 36 catccgaaac atcacaaaac agacgcagtc caaatagac gtgcatagga aggagaatgc 840
 37 gggcgctgcg gagaaggcca tcagcgtgca ttcaaccct gaaggctgtc cctccgcgtg 900
 38 caagatgac ttggagatta tgcacaagga ggcaaggac accaaaacgg cagatgaagt 960
 39 tcccctgaag atcctggctc ataacaactt cgtcgggcca ctcatggca aggaaggccg 1020
 40 gaacctgaag aaggtggagc aggacacaga gacgaagatc accatctcat cgtccagga 1080
 41 cctcacgctc tataaccctg agaggacct cactgtgaag ggcgccattg agaactgttg 1140
 42 cagggccgag caggagatca tgaagaaagt tcgagaggct tacgagaacg acgtggccgc 1200
 43 catgagcttg cagtcccacc tcatccttg gcttaacctg gctgctgtag gtctcttccc 1260
 44 agcttcatcc agcgtgtgct ctctcctcc cagcagtgtc actggggctg ctccctatag 1320
 45 ctcttcatg caggctccgg agcaggagat ggtacaagtg ttcacccccg cccaggctgt 1380
 46 gggcgccatc attggcaaga agggccagca catcaaaca ctctcccgtt tcgccagcgc 1440
 47 ctccatcaag attgctccac cagaaacacc tgactccaaa gttcgaatgg tcgtcatcac 1500
 48 tggaccccca gaggtcagt tcaaggctca gggaagaatt tatggcaaac taaaagaaga 1560
 49 gaatttcttt ggtcccaagg aggaagtaaa gctagagacc cacatacggg ttccggcttc 1620
 50 agcagccggc cgcgtcatcg gcaaaggcgg caaacgggtg aatgagctgc agaacttgac 1680
 51 tgcagctgag gtggtagtgc caagagacca gaccccgat gagaacgacc aagtcattgt 1740
 52 taagatcatc ggacatttct atgccagcca gatggctcag cggaagatcc gagacatcct 1800
 53 ggctcaagtt aagcaacagc accagaaggg acagagcaac ctggcccagg cacggaggaa 1860
 54 gtgaccccgcc cccctcctgt cccattggct ccaagatcag caggaggaaac acagaactgg 1920
 55 aggggcccgg ggaggccgg tgtgtttttc ccagcaggcc tgagaatgag tgggaatcag 1980
 56 ggcatttggt cctggctgga gatcagggtt gcacactgta ttgagaacaa tgttccagtg 2040

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```

57 aggaatcctg atctctcgcc cccaattgag ccagctggcc acagcccacc ccttggaata 2100
58 tcaccattgc aatcatagct tgggttgctt ttaaactgtg attgtcttga agttctccag 2160
59 cctccatgga aggatgggtc agatcccagt ggggaagaga aataaaattt ccttcagggt 2220
60 ttat 2224
62 <210> SEQ ID NO: 2
63 <211> LENGTH: 577
64 <212> TYPE: PRT
65 <213> ORGANISM: Mus musculus
67 <400> SEQUENCE: 2
68 Met Asn Lys Leu Tyr Ile Gly Asn Leu Asn Glu Ser Val Thr Pro Ala
69 1 5 10 15
71 Asp Leu Glu Lys Val Phe Ala Glu His Lys Ile Ser Tyr Ser Gly Gln
72 20 25 30
74 Phe Leu Val Lys Ser Gly Tyr Ala Phe Val Asp Cys Pro Asp Glu His
75 35 40 45
77 Trp Ala Met Lys Ala Ile Glu Thr Phe Ser Gly Lys Val Glu Leu Gln
78 50 55 60
80 Gly Lys Arg Leu Glu Met Glu His Ser Val Pro Lys Lys Gln Arg Ser
81 65 70 75 80
83 Arg Lys Ile Gln Ile Arg Asn Ile Pro Pro Gln Leu Arg Trp Glu Val
84 85 90 95
86 Leu Asp Ser Leu Leu Ala Gln Tyr Gly Thr Val Glu Asn Cys Glu Gln
87 100 105 110
89 Val Asn Thr Glu Ser Glu Thr Ala Val Val Asn Val Thr Tyr Ser Asn
90 115 120 125
92 Arg Glu Gln Thr Arg Gln Ala Ile Met Lys Leu Asn Gly His Gln Leu
93 130 135 140
95 Glu Asn His Ala Leu Lys Val Ser Tyr Ile Pro Asp Glu Gln Ile Thr
96 145 150 155 160
98 Gln Gly Pro Glu Asn Gly Arg Arg Gly Gly Phe Gly Ser Arg Gly Gln
99 165 170 175
101 Pro Arg Gln Gly Ser Pro Val Ala Ala Gly Ala Pro Ala Lys Gln Gln
102 180 185 190
104 Pro Val Asp Ile Pro Leu Arg Leu Leu Val Pro Thr Gln Tyr Val Gly
105 195 200 205
107 Ala Ile Ile Gly Lys Glu Gly Ala Thr Ile Arg Asn Ile Thr Lys Gln
108 210 215 220
110 Thr Gln Ser Lys Ile Asp Val His Arg Lys Glu Asn Ala Gly Ala Ala
111 225 230 235 240
113 Glu Lys Ala Ile Ser Val His Ser Thr Pro Glu Gly Cys Ser Ser Ala
114 245 250 255
116 Cys Lys Met Ile Leu Glu Ile Met His Lys Glu Ala Lys Asp Thr Lys
117 260 265 270
119 Thr Ala Asp Glu Val Pro Leu Lys Ile Leu Ala His Asn Asn Phe Val
120 275 280 285
122 Gly Arg Leu Ile Gly Lys Glu Gly Arg Asn Leu Lys Lys Val Glu Gln
123 290 295 300
125 Asp Thr Glu Thr Lys Ile Thr Ile Ser Ser Leu Gln Asp Leu Thr Leu
126 305 310 315 320

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```

128 Tyr Asn Pro Glu Arg Thr Ile Thr Val Lys Gly Ala Ile Glu Asn Cys
129                               325                               330                               335
131 Cys Arg Ala Glu Gln Glu Ile Met Lys Lys Val Arg Glu Ala Tyr Glu
132                               340                               345                               350
134 Asn Asp Val Ala Ala Met Ser Leu Gln Ser His Leu Ile Pro Gly Leu
135                               355                               360                               365
137 Asn Leu Ala Ala Val Gly Leu Phe Pro Ala Ser Ser Ser Ala Val Pro
138                               370                               375                               380
140 Pro Pro Pro Ser Ser Val Thr Gly Ala Ala Pro Tyr Ser Ser Phe Met
141 385                               390                               395                               400
143 Gln Ala Pro Glu Gln Glu Met Val Gln Val Phe Ile Pro Ala Gln Ala
144                               405                               410                               415
146 Val Gly Ala Ile Ile Gly Lys Lys Gly Gln His Ile Lys Gln Leu Ser
147                               420                               425                               430
149 Arg Phe Ala Ser Ala Ser Ile Lys Ile Ala Pro Pro Glu Thr Pro Asp
150                               435                               440                               445
152 Ser Lys Val Arg Met Val Val Ile Thr Gly Pro Pro Glu Ala Gln Phe
153                               450                               455                               460
155 Lys Ala Gln Gly Arg Ile Tyr Gly Lys Leu Lys Glu Glu Asn Phe Phe
156 465                               470                               475                               480
158 Gly Pro Lys Glu Glu Val Lys Leu Glu Thr His Ile Arg Val Pro Ala
159                               485                               490                               495
161 Ser Ala Ala Gly Arg Val Ile Gly Lys Gly Gly Lys Thr Val Asn Glu
162                               500                               505                               510
164 Leu Gln Asn Leu Thr Ala Ala Glu Val Val Val Pro Arg Asp Gln Thr
165                               515                               520                               525
167 Pro Asp Glu Asn Asp Gln Val Ile Val Lys Ile Ile Gly His Phe Tyr
168                               530                               535                               540
170 Ala Ser Gln Met Ala Gln Arg Lys Ile Arg Asp Ile Leu Ala Gln Val
171 545                               550                               555                               560
173 Lys Gln Gln His Gln Lys Gly Gln Ser Asn Leu Ala Gln Ala Arg Arg
174                               565                               570                               575
176 Lys

```

180 <210> SEQ ID NO: 3

181 <211> LENGTH: 14

182 <212> TYPE: PRT

183 <213> ORGANISM: Mus musculus

185 <400> SEQUENCE: 3

186 Arg Arg Gly Gly Phe Gly Ser Arg Gly Gln Pro Arg Gln Gly

187 1 5 10

190 <210> SEQ ID NO: 4

191 <211> LENGTH: 14

192 <212> TYPE: PRT

193 <213> ORGANISM: Homo sapiens

195 <400> SEQUENCE: 4

196 Gly Arg Arg Gly Leu Gly Gln Arg Gly Ser Ser Arg Gln Gly

197 1 5 10

200 <210> SEQ ID NO: 5

201 <211> LENGTH: 14

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```

202 <212> TYPE: PRT
203 <213> ORGANISM: Homo sapiens
205 <400> SEQUENCE: 5
206 Gly Arg Gly Gly Phe Asp Arg Met Pro Pro Gly Arg Gly Gly
207   1               5               10
210 <210> SEQ ID NO: 6
211 <211> LENGTH: 13
212 <212> TYPE: PRT
213 <213> ORGANISM: Homo sapiens
215 <400> SEQUENCE: 6
216 Gly Arg Gly Gly Phe Gly Asp Arg Gly Gly Arg Gly Gly
217   1               5               10
220 <210> SEQ ID NO: 7
221 <211> LENGTH: 14
222 <212> TYPE: PRT
223 <213> ORGANISM: Homo sapiens
225 <400> SEQUENCE: 7
226 Gly Arg Gly Gly Phe Gly Gly Arg Gly Gly Gly Arg Gly Gly
227   1               5               10
230 <210> SEQ ID NO: 8
231 <211> LENGTH: 14
232 <212> TYPE: PRT
233 <213> ORGANISM: Homo sapiens
235 <400> SEQUENCE: 8
236 Leu Arg Arg Gly Asp Gly Arg Arg Arg Gly Gly Gly Arg Gly
237   1               5               10
240 <210> SEQ ID NO: 9
241 <211> LENGTH: 13
242 <212> TYPE: PRT
243 <213> ORGANISM: Artificial Sequence
245 <220> FEATURE:
246 <223> OTHER INFORMATION: Consensus sequence for SEQ ID NOs:3-8.
248 <400> SEQUENCE: 9
249 Gly Arg Gly Gly Phe Gly Arg Gly Gly Gly Arg Gly Gly
250   1               5               10
253 <210> SEQ ID NO: 10
254 <211> LENGTH: 11
255 <212> TYPE: PRT
256 <213> ORGANISM: Mus musculus
258 <400> SEQUENCE: 10
259 Gln Leu Arg Trp Glu Val Leu Asp Ser Leu Leu
260   1               5               10
263 <210> SEQ ID NO: 11
264 <211> LENGTH: 11
265 <212> TYPE: PRT
266 <213> ORGANISM: Homo sapiens
268 <400> SEQUENCE: 11
269 His Leu Gln Trp Glu Val Leu Asp Ser Leu Leu
270   1               5               10

```

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Input Set : A:\Jeffrey.app

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```

273 <210> SEQ ID NO: 12
274 <211> LENGTH: 10
275 <212> TYPE: PRT
276 <213> ORGANISM: Homo sapiens
278 <400> SEQUENCE: 12
279 Gln Leu Arg Leu Glu Arg Leu Gln Ile Asp
280   1               5               10
283 <210> SEQ ID NO: 13
284 <211> LENGTH: 11
285 <212> TYPE: PRT
286 <213> ORGANISM: Homo sapiens
288 <400> SEQUENCE: 13
289 Thr Ile Ser Ser Leu Gln Asp Leu Thr Leu Tyr
290   1               5               10
293 <210> SEQ ID NO: 14
294 <211> LENGTH: 11
295 <212> TYPE: PRT
296 <213> ORGANISM: Homo sapiens
298 <400> SEQUENCE: 14
299 Thr Ile Ser Pro Leu Gln Glu Leu Thr Leu Tyr
300   1               5               10
303 <210> SEQ ID NO: 15
304 <211> LENGTH: 11
305 <212> TYPE: PRT
306 <213> ORGANISM: Human immunodeficiency virus
308 <400> SEQUENCE: 15
309 Gln Leu Pro Pro Leu Glu Arg Leu Thr Leu Asp
310   1               5               10
313 <210> SEQ ID NO: 16
314 <211> LENGTH: 7
315 <212> TYPE: PRT
316 <213> ORGANISM: Artificial Sequence
318 <220> FEATURE:
319 <223> OTHER INFORMATION: Consensus sequence for SEQ ID NOS:10-15.
321 <400> SEQUENCE: 16
322 Gln Leu Leu Glu Leu Thr Leu
323   1               5
326 <210> SEQ ID NO: 17
327 <211> LENGTH: 47
328 <212> TYPE: PRT
329 <213> ORGANISM: Mus musculus
331 <400> SEQUENCE: 17
332 Leu Leu Val Pro Thr Gln Tyr Val Gly Ala Ile Ile Gly Lys Glu Gly
333   1               5               10               15
335 Ala Thr Ile Arg Asn Ile Thr Lys Gln Thr Gln Ser Lys Ile Asp Val
336           20               25               30
338 His Arg Lys Glu Asn Ala Gly Ala Ala Glu Lys Ala Ile Ser Val
339           35               40               45
342 <210> SEQ ID NO: 18

```



Use of n and/or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to insure a corresponding explanation is presented in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

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L:10 M:270 C: Current Application Number differs, Replaced Application Number

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:750 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45